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PCT10

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/088,202

DATE: 03/28/2002 Errors on pp. 1-4
TIME: 14:04:31

Input Set : A:\PTO.PG.txt
Output Set: N:\CRF3\03282002\J088202.raw

3 <110> APPLICANT: MOGAM BIOTECHNOLOGY RESEARCH INSTITUTE
5 <120> TITLE OF INVENTION: NOVEL DETOXIFIED MUTANTS OF Escherichia coli HEAT-LABILE
6 ENTEROTOXIN
8 <130> FILE REFERENCE: 2p-03-12
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/088,202
C--> 10 <141> CURRENT FILING DATE: 2002-03-15
10 <160> NUMBER OF SEQ ID NOS: 6
12 <170> SOFTWARE: KopatentIn 1.71

ERRORRED SEQUENCES

40 <210> SEQ ID NO: 3
 41 <211> LENGTH: 382
 42 <212> TYPE: PRT
 43 <213> ORGANISM: Escherichia coli
 45 <220> FEATURE:
 46 <221> NAME/KEY: SIGNAL
 47 <222> LOCATION: (-18)..(-1)
 49 <400> SEQUENCE: 3
 50 Met Lys Asn Ile Thr Phe Ile Phe Phe Ile Leu Leu Ala Ser Pro Leu
 51 -18 -14 -9
 52 -4
 54 Tyr Ala Asn Gly Asp Arg Leu Tyr Arg Ala Asp Ser Arg Pro Pro Asp
 55 2 7 104 4000. George 12
 57 Glu Ile Lys Arg Ser Gly Gly Leu Met Pro Arg Gly His Asn Glu Tyr Ala Asn Gly Asp Arg
 58 17 22 27 196 199 -14
 60 Phe Asp Arg Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg Tyr Ala Asn Gly Asp Arg
 61 32 37 42 199 2
 63 Gly Thr Gln Thr Gly Phe Val Arg Tyr Asp Asp Gly Tyr Val Ser Thr Ile Lys Arg Ser Gly Asp Arg
 64 47 52 57 2062 17
 66 Tyr Leu Ser Leu Arg Ser Ala His Leu Ala Gly Gln Ser Ile Leu Ser Asp Arg Gly Thr Gly Met
 67 67 72 77205 32 3
 69 Gly Tyr Ser Thr Tyr Tyr Ile Tyr Val Ile Ala Thr Ala Pro Asn Met Thr Gln Thr Gly Phe Val
 70 82 87 92 208 47 52
 72 Phe Asn Val Asn Asp Val Leu Gly Val Tyr Ser Pro His Pro Tyr Glu Ser Leu Arg Ser Al
 73 97 102 107 311 67
 75 Gln Glu Val Ser Ala Leu Gly Gly Ile Pro Tyr Ser Gln Ile Tyr Gly Tyr Ser Ser Thr Tyr Val
 76 112 117 122 214 32
 78 Trp Tyr Arg Val Asn Phe Gly Val Ile Asp Glu Arg Leu His Arg Asn Val Val Asn Asp Val
 79 127 132 137 142
 81 Arg Glu Tyr Arg Asp Arg Tyr Tyr Arg Asn Leu Asn Ile Ala Pro Ala
 82 147 152 157

Misalignment of amino acid
Numbering: See error summary
Sheet item 3.

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84 Glu Asp Gly Tyr Arg Leu Ala Gly Phe Pro Pro Asp His Gln Ala Trp
E--> 85 162 167 172
87 Arg Glu Glu Pro Trp Ile His His Ala Pro Gln Gly Cys Gly Asn Ser
E--> 88 177 182 187
90 Ser Arg Thr Ile Thr Gly Asp Thr Cys Asn Glu Glu Thr Gln Asn Leu
E--> 91 192 197 202
93 Ser Thr Ile Tyr Leu Arg Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile
E--> 94 207 212 217 222
96 Phe Ser Asp Tyr Gln Ser Glu Val Asp Ile Tyr Asn Arg Ile Arg Asp
E--> 97 227 232 237
99 Glu Leu Met Asn Lys Val Lys Phe Tyr Val Leu Phe Thr Ala Leu Leu
E--> 100 242 247 252
102 Ser Ser Leu Cys Ala His Gly Ala Pro Gln Ser Ile Thr Glu Leu Cys
E--> 103 257 262 267
105 Ser Glu Tyr His Asn Thr Gln Ile Tyr Thr Ile Asn Asp Lys Ile Leu
E--> 106 272 277 282
108 Ser Tyr Thr Glu Ser Met Ala Gly Lys Arg Glu Met Val Ile Ile Thr
E--> 109 287 292 297 302
111 Phe Lys Ser Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln His
E--> 112 307 312 317
114 Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg
E--> 115 322 327 332
117 Ile Thr Tyr Leu Thr Glu Thr Lys Ile Asp Lys Leu Cys Val Trp Asn
E--> 118 337 342 347
120 Asn Lys Thr Pro Asn Ser Ile Ala Ala Ile Ser Met Glu Asn
E--> 121 352 357 362
185 <210> SEQ ID NO: 5
186 <211> LENGTH: 380
187 <212> TYPE: PRT
188 <213> ORGANISM: Escherichia coli
190 <220> FEATURE:
191 <221> NAME/KEY: SIGNAL
192 <222> LOCATION: (-18)..(-1)
194 <400> SEQUENCE: 5
195 Met Lys Asn Ile Thr Phe Ile Phe Phe Ile Leu Leu Ala Ser Pro Leu
196 -18 -14 -9 -470 <212> TYPE: DNA
198 Tyr Ala Asn Gly Asp Arg Leu Tyr Arg Ala Asp Ser Arg Pro Pro Asp
E--> 199 2 7 12 273 <400> SEQUENCE: 6
201 Glu Ile Lys Arg Ser Gly Gly Leu Met Pro Arg Gly His Asn Glu Tyr
E--> 202 17 22 27 276
204 Phe Asp Arg Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg
E--> 205 32 37 42 780
207 Gly Thr Gln Thr Gly Phe Val Arg Tyr Asp Asp Gly Tyr Val Ser Thr
E--> 208 47 52 57 7462
210 Ser Leu Ser Leu Arg Ser Ala His Leu Ala Gly Gln Ser Ile Leu Ser
E--> 211 67 72 7738
213 Gly Tyr Ser Thr Tyr Tyr Ile Tyr Val Ile Ala Thr Ala Pro Asn Met
E--> 214 82 87 92 892
216 Phe Asn Val Asn Asp Val Leu Gly Val Tyr Ser Pro His Pro Tyr Gln

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E--> 217 97 102 107
219 Val Ser Ala Leu Gly Gly Ile Pro Tyr Ser Gln Ile Tyr Gly Trp Tyr
E--> 220 112 117 122
222 Arg Val Asn Phe Gly Val Ile Asp Glu Arg Leu His Arg Asn Arg Glu
E--> 223 127 132 137 142
225 Tyr Arg Asp Arg Tyr Tyr Arg Asn Leu Asn Ile Ala Pro Ala Glu Asp
E--> 226 147 152 157
228 Gly Tyr Arg Leu Ala Gly Phe Pro Pro Asp His Gln Ala Trp Arg Glu
E--> 229 162 167 172
231 Glu Pro Trp Ile His His Ala Pro Gln Gly Cys Gly Asn Ser Ser Arg
E--> 232 177 182 187
234 Thr Ile Thr Gly Asp Thr Cys Asn Glu Glu Thr Gln Asn Leu Ser Thr
E--> 235 192 197 202
237 Ile Tyr Leu Arg Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser
E--> 238 207 212 217 222
240 Asp Tyr Gln Ser Glu Val Asp Ile Tyr Asn Arg Ile Arg Asp Glu Leu
E--> 241 227 232 237
243 Met Asn Lys Val Lys Phe Tyr Val Leu Phe Thr Ala Leu Leu Ser Ser
E--> 244 242 247 252
246 Leu Cys Ala His Gly Ala Pro Gln Ser Ile Thr Glu Leu Cys Ser Glu
E--> 247 257 262 267
249 Tyr His Asn Thr Gln Ile Tyr Thr Ile Asn Asp Lys Ile Leu Ser Tyr
E--> 250 272 277 282
252 Thr Glu Ser Met Ala Gly Lys Arg Glu Met Val Ile Ile Thr Phe Lys
E--> 253 287 292 297 302
255 Ser Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp
E--> 256 307 312 317
258 Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Thr
E--> 259 322 327 332
261 Tyr Leu Thr Glu Thr Lys Ile Asp Lys Leu Cys Val Trp Asn Asn Lys
E--> 262 337 342 347
264 Thr Pro Asn Ser Ile Ala Ala Ile Ser Met Glu Asn
E--> 265 352 357 362
268 <210> SEQ ID NO: 6
269 <211> LENGTH: 1508
270 <212> TYPE: DNA
271 <213> ORGANISM: Escherichia coli
273 <400> SEQUENCE: 6
274 ggatccgtgc actcttctt tatcgcttca ctacacattt tattcctcgca tggatgtttt 60
276 ataaaaaaca tgattgacat catgttgcatt ataggttaaa caaaaacaagt ggcgttatct 120
278 tttccggat tgcattttttt tatgtatataat aagttttcct cgaatggaaa atataacttt 180
280 catttttttt attttattag catgcattt atatgcattt ggcgacagat tataccgtgc 240
282 tgactctaga cccccagatg aaataaaacg ttccggaggt cttatgcctt gagggctaa 300
284 tgacttgc gatagaggaa ctcaaatgaa tattatctt tatgtatcag cgagagggaaac 360
286 acaaacggc tttgtcagat atgatgacgg atatgttcc acttcttca gtttggagaag 420
288 tgctcaacttgc gcaaggacatg ctatattatc aggatattcc acttactata tataatgttat 480
290 agcagacagca ccaaatatgt ttaatgtttaa tgatgtttaa ggcgtataca gccctcacc 540
292 atatcagggt tctgcgttag gtggaaatacc atattcttag atatatgtat ggtatcgtgt 600
294 taattttgggt gtgatttgatg aacgattaca tcgtaacagg gaatataagag accggattta 660

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296	cagaaaatctg	aatatagctc	cggcagagga	tggttacaga	ttagcaggtt	tcccaccgga	720
298	tcaccaagct	tggagagaag	aaccctggat	tcatcatgca	ccacaagggt	gtgaaattc	780
300	atcaagaaca	atcacaggtg	atacttgtaa	tgaggagacc	cagaatctga	gcacaatata	840
302	tctcaggaa.	tatcaatcaa	aagttaagag	gcagatattt	ttagactatc	agtcagaggt	900
304	tgacatatat	aacagaattc	gggatgaatt	atgaataaag	taaaatttt	tgttttattt	960
306	acggcgttac	tatcctctct	atgtgcacac	ggagctcctc	agtcttattac	agaactatgt	1020
308	tcgaaatatc	acaacacaca	aatatatacg	ataaaatgaca	agatactatc	atatacggaa	1080
310	tcgatggcag	gcaaaaagaga	aatggtttac	attacattt	agagcggcgc	aacatttcag	1140
312	gtcgaagtcc	cgggcagtca	acatatagac	tcccaaaaaa	aagccattga	aaggatgaag	1200
314	gacacattaa	gaatcacata	tctgaccggag	acccaaaattt	ataaattatg	tgtatggaat	1260
316	aataaaaccc	ccaattcaat	tgcggcaatc	agtatggaaa	actagttgc	ttaaaagca	1320
318	tgtctaatgc	taggaaccta	tataacaact	actgtactta	tactaatgag	ccttatgctg	1380
320	catttgaaaa	ggcggttagag	gatgcaatac	cgatcctaa	actgtaaacac	tataacagct	1440
322	tccactacag	ggagctgttta	tagcaaacag	aaaaaactaa	gctaggctgg	aggggcaagc	1500
324	tttgatcc						1508

E--> 325 1

E--> 329 1

delete

VERIFICATION SUMMARY

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Input Set: A:\PTO.PG.txt

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:51 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
M:332 Repeated in SeqNo=3
L:199 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5
M:332 Repeated in SeqNo=5
L:325 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:1508 SEQ:6
M:254 Repeated in SeqNo=6